

Abstract of the Disclosure

The invention relates to a compound that competitively inhibits binding of CSP to *S. mutans* histidine kinase. The compound is preferably a peptide or an antibody. The compound is preferably a derivative of [SEQ ID NO:2], a fragment of [SEQ ID NO:2] or a derivative of a fragment of [SEQ ID NO:2].

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SEQUENCE LISTING

<110> CVITKOVITCH, Dennis

<120> SIGNAL PEPTIDES NUCLEIC ACID MOLECULES AND METHODS FOR TREATMENT OF CARIES

<130> 311/0003

<140> 2 302 861

<141> 2000-04-10

<160> 28

<170> PatentIn version 3.0

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Asp	Glu	Leu	Glu	Ile	Ile	Ile	Gly	Gly	Ser	Gly	Ser	Leu	Ser	Thr	Phe	
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ttc	cgg	ctg	ttt	aac	aga	agt	ttt	aca	caa	gct	ttg	gga	aaa	taa	141
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1 5 10 15	

acc gtt cta ttt ctc ttg ttt cta ttt tct aag gta agt aat gtc act	96
Thr Val Leu Phe Leu Leu Phe Leu Phe Ser Lys Val Ser Asn Val Thr	
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tta tcg aaa aag gaa tta act ctt ttt tcg ata agc aat ttt ctg ata	144
Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile	
35 40 45	

atg att gct gtt acg atg gtg aac gta aac ctg ttt tat cct gca gag	192
Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu	
50 55 60	

cct ctt tat ttt ata gct tta tca att tat ctt aat aga cag aat agt	240
Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser	
65 70 75 80	

ctt tct cta aat ata ttt tat ggt ctg ctg cct gtt gcc agt tct gac	288
Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp	
85 90 95	

ttg ttt agg cgg gca atc ata ttc ttt atc ttg gat gga act caa gga	336
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Ile	Val	Met	Gly	Ser	Ser	Ile	Ile	Thr	Thr	Tyr	Met	Ile	Glu	Phe	Ala	
		115					120					125				
gga	ata	gcg	cta	agt	tac	ctc	ttt	ctc	agt	gtg	ttc	aat	ggt	gat	att	432
Gly	Ile	Ala	Leu	Ser	Tyr	Leu	Phe	Leu	Ser	Val	Phe	Asn	Val	Asp	Ile	
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Gln	Lys	Glu	Ala	Gln	Ile	Arg	Asn	Ile	Thr	Gln	Tyr	Ser	Gln	Gln	Ile	
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Glu	Ser	Leu	Tyr	Lys	Asp	Ile	Arg	Ser	Phe	Arg	His	Asp	Tyr	Leu	Asn	
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Gln	Asp	Thr	Arg	Tyr	Asn	Ile	Gly	His	Leu	Ala	Asn	Ile	Gln	Asn	Asp	
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325	330	335	
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Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn			
340	345	350	
gcc att gag gct gct ttc gaa tca tta aat cct gaa att cag tta gcc			1104
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355	360	365	
ttt ttt aag aaa aat ggc agt ata gtc ttt atc att cag aat tcc acc			1152
Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr			
370	375	380	
aaa gaa aaa caa ata gat gtg agt aaa att ttt aaa gaa aac tat tcc			1200
Lys Glu Lys Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser			
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Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile			
405	410	415	
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Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser
65 70 75 80

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85 90 95

Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly
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Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala
115 120 125

Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile
130 135 140

Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu
145 150 155 160

Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val
165 170 175

Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg
180 185 190

Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser
195 200 205

Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala
210 215 220

Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile
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Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn
245 250 255

Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser
260 265 270

Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu
275 280 285

Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp
290 295 300

Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys
305 310 315 320

Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu
325 330 335

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340 345 350

Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala
355 360 365

Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr
370 375 380

Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser
385 390 395 400

Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
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1 5 10 15	
ctt gaa acc acc att gca gct atc atg aaa gaa aaa aat tgg tct tat	96
Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr	
20 25 30	
aaa gaa ttg act att ttt gga aaa cca caa caa ctt att gac gct atc	144
Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile	
35 40 45	
cct gaa aag ggc aat cac cag att ttc ttt ttg gat att gaa atc aaa	192
Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys	
50 55 60	
aaa gag gaa aag aaa gga ctg gaa gta gcc aat cag att aga cag cat	240
Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His	
65 70 75 80	
aat cct agt gca gtt att gtc ttt gtc acg aca cat tct gag ttt atg	288
Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met	
85 90 95	
ccc ctc act ttt cag tat cag gta tct gct ttg gat ttt att gat aaa	336
Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys	
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Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr	
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Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe	
130 135 140	
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Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile	
145 150 155 160	
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Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr	
165 170 175	
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Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys	
180 185 190	
atg gat aag aga ctt ttt cag tgc cat cgc tct ttt att gtc aat cct	624
Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro	
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Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile
145 150 155 160

Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr
165 170 175

Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys
180 185 190

Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro
195 200 205

Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg
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tgg aaa tta agc cgt tat tac ttt att aaa atg tgg act cgt gaa gat 96
Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp
20 25 30

tgg caa caa gag gga atg ttg att ttg cac caa tta tta agg gaa cat 144
Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His
35 40 45

cca gaa tta gaa gag gat gat aca aaa ttg tat atc tat ttt aag aca 192
Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr
50 55 60

cgt ttt tct aat tac att aaa gat gtt ttg cgt cag caa gaa agt cag 240
Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln
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aaa cgt cgt ttt aat aga atg tct tat gaa gaa gtc ggt gag att gaa 288
Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu
85 90 95

cac tgt ttg tca agt ggc ggt atg caa ttg gat gaa tat att tta ttt 336
His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe
100 105 110

cgt gat agt ttg ctt gca tat aaa caa ggt ctg agt act gaa aag caa 384
Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln
115 120 125

gag ctg ttt gag cgc ttg gta gca ggagagcact ttttggaag gcaaagtatg 438
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35 40 45

Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr
50 55 60

Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln
65 70 75 80

Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu
85 90 95

His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe
100 105 110

Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln
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tgtttttaaat aagggttaagc caattgtatg gaaattaagc cgttattact ttattaaaaat 180
gtggactcgt gaagattggc aacaagaggg aatgttgatt ttgcaccaat tattaaggga 240
acatccagaa ttagaagagg atgatacaaa attgtatatc tattttaaga cacgtttttc 300
taattacatt aaagatgttt tgcgtcagca agaaagtcag aaacgtcgtt ttaatagaat 360
gtcttatgaa gaagtcggtg agattgaaca ctgtttgtca agtggcggta tgcaattgga 420
tgaatatatt ttatttcgtg atagtttgct tgcataataa caaggctctga gtactgaaaa 480
gcaagagctg tttgagcgtg tggtagcagg agagcacttt ttgggaaggc aaagtatgct 540
gaaagattta cgtaaaaaat taagtgattt taaggaaaaa tagttaaaaa gggaaagaat 600
ggaacatgtg attgtacat tctttttggt tgaaaattaa gaaaagttat tataaattat 660
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<210> 25

<211> 2280

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1) .. (2280)

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1 5 10 15

ctc tta gag att atc aaa aga gta aca aaa agg gga ggg aca gtt tcg 96
Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser
20 25 30

tca tct aat cct tta cca gat ggg cag tct aag ttg ttt tgg cgc aga 144
Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg
35 40 45

cat tat aag cta gta cct cag att gat acc aga gac tgt ggg ccg gca 192
His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala
50 55 60

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gtg ctg gca tct gtt gca aag cat tac gga tct aat tac tct atc gct Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala 65 70 75 80	240
tat ctg cgg gaa ctc tca aag act aac aag cag gga aca aca gct ctt Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu 85 90 95	288
ggc att gtt gaa gct gct aaa aag tta ggc ttt gaa aca cgc tct atc Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile 100 105 110	336
aag gcg gat atg acg ctt ttt gat tat aat gat ttg acc tat cct ttt Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe 115 120 125	384
atc gtc cat gtg att aaa gga aaa cgt ctg cag cat tat tat gtc gtc Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val 130 135 140	432
tat ggc agc cag aat aat cag ctg att att gga gat cct gat cct tca Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser 145 150 155 160	480
gtt aag gtg act agg atg agt aag gaa cgc ttt caa tca gag tgg aca Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr 165 170 175	528
ggc ctt gca att ttc cta gct cct cag cct aac tat aag cct cat aaa Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys 180 185 190	576
ggt gaa aaa aat ggt ttg tct aat ttc ttc ccg ttg atc ttt aag cag Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln 195 200 205	624
aaa gct ttg atg act tat att atc ata gct agc ttg att gtg acg ctc Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu 210 215 220	672
att gat att gtc gga tca tac tat ctc caa gga ata ttg gac gag tac Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr 225 230 235 240	720
att cct gat cag ctg att tca act tta gga atg att acg att ggt ctg Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu 245 250 255	768
ata ata acc tat att atc cag cag gtc atg gct ttt gca aaa gaa tac Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr 260 265 270	816
ctc ttg gcc gta ctc agt ttg cgt tta gtc att gat gtt atc ctg tct Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser 275 280 285	864
tat atc aaa cat att ttt acg ctt cct atg tct ttc ttt gcg aca agg	912

Tyr	Ile	Lys	His	Ile	Phe	Thr	Leu	Pro	Met	Ser	Phe	Phe	Ala	Thr	Arg		
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cga	aca	gga	gaa	atc	acg	tct	cgt	ttt	aca	gat	gcc	aat	cag	att	att	960	
Arg	Thr	Gly	Glu	Ile	Thr	Ser	Arg	Phe	Thr	Asp	Ala	Asn	Gln	Ile	Ile		
305					310					315					320		
gat	gct	gta	gcg	tca	acc	atc	ttt	tca	atc	ttt	tta	gat	atg	act	atg	1008	
Asp	Ala	Val	Ala	Ser	Thr	Ile	Phe	Ser	Ile	Phe	Leu	Asp	Met	Thr	Met		
				325					330					335			
gta	att	ttg	gtt	ggg	ggg	gtt	ttg	ttg	gcg	caa	aac	aat	aac	ctt	ttc	1056	
Val	Ile	Leu	Val	Gly	Gly	Val	Leu	Leu	Ala	Gln	Asn	Asn	Asn	Leu	Phe		
			340					345					350				
ttt	cta	acc	ttg	ctc	tcc	att	ccg	att	tat	gcc	atc	att	att	ttt	gct	1104	
Phe	Leu	Thr	Leu	Leu	Ser	Ile	Pro	Ile	Tyr	Ala	Ile	Ile	Ile	Phe	Ala		
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ttc	ttg	aaa	ccc	ttt	gag	aaa	atg	aat	cac	gaa	gtg	atg	gaa	agc	aat	1152	
Phe	Leu	Lys	Pro	Phe	Glu	Lys	Met	Asn	His	Glu	Val	Met	Glu	Ser	Asn		
		370				375					380						
gct	gtg	gta	agt	tct	tct	atc	att	gaa	gat	atc	aat	ggg	atg	gaa	acc	1200	
Ala	Val	Val	Ser	Ser	Ser	Ile	Ile	Glu	Asp	Ile	Asn	Gly	Met	Glu	Thr		
385					390					395					400		
att	aaa	tca	ctc	aca	agt	gag	tcc	gct	cgt	tat	caa	aac	att	gat	agt	1248	
Ile	Lys	Ser	Leu	Thr	Ser	Glu	Ser	Ala	Arg	Tyr	Gln	Asn	Ile	Asp	Ser		
			405					410						415			
gaa	ttt	gtt	gat	tat	ttg	gag	aaa	aac	ttt	aag	cta	cac	aag	tat	agt	1296	
Glu	Phe	Val	Asp	Tyr	Leu	Glu	Lys	Asn	Phe	Lys	Leu	His	Lys	Tyr	Ser		
			420				425						430				
gcc	att	caa	acc	gca	tta	aaa	agc	ggg	gct	aag	ctt	atc	ctc	aat	gtt	1344	
Ala	Ile	Gln	Thr	Ala	Leu	Lys	Ser	Gly	Ala	Lys	Leu	Ile	Leu	Asn	Val		
		435				440						445					
gtc	att	ctc	tgg	tat	ggc	tct	cgt	cta	gtt	atg	gat	aat	aaa	atc	tca	1392	
Val	Ile	Leu	Trp	Tyr	Gly	Ser	Arg	Leu	Val	Met	Asp	Asn	Lys	Ile	Ser		
	450				455						460						
gtt	ggg	cag	ctt	atc	acc	ttt	aat	gct	ttg	ctg	tct	tat	ttc	tca	aat	1440	
Val	Gly	Gln	Leu	Ile	Thr	Phe	Asn	Ala	Leu	Leu	Ser	Tyr	Phe	Ser	Asn		
465					470					475					480		
cca	att	gaa	aat	att	atc	aat	ctg	caa	tcc	aaa	ctg	cag	tca	gct	cgc	1488	
Pro	Ile	Glu	Asn	Ile	Ile	Asn	Leu	Gln	Ser	Lys	Leu	Gln	Ser	Ala	Arg		
			485					490						495			
gtt	gcc	aat	aca	cgt	ctt	aat	gag	gtc	tat	ctt	gtc	gaa	tct	gaa	ttt	1536	
Val	Ala	Asn	Thr	Arg	Leu	Asn	Glu	Val	Tyr	Leu	Val	Glu	Ser	Glu	Phe		
		500					505					510					
gaa	aaa	gac	ggc	gat	tta	tca	gaa	aat	agc	ttt	tta	gat	ggg	gat	att	1584	
Glu	Lys	Asp	Gly	Asp	Leu	Ser	Glu	Asn	Ser	Phe	Leu	Asp	Gly	Asp	Ile		

515	520	525	
tcg ttt gaa aat ctt tct tat aaa tat gga ttt ggg cga gat acc tta Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu 530 535 540			1632
tca gat att aat tta tca atc aaa aaa ggc tcc aag gtc agt cta gtt Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val 545 550 555 560			1680
gga gcc agt ggt tct ggt aaa aca act ttg gct aaa ctg att gtc aat Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn 565 570 575			1728
ttc tac gag cct aac aag ggg att gtt cga atc aat ggc aat gat tta Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu 580 585 590			1776
aaa gtt att gat aag aca gct ttg cgg cgg cat att agc tat ttg ccg Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro 595 600 605			1824
caa cag gcc tat gtt ttt agt ggc tct att atg gat aat ctc gtt tta Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu 610 615 620			1872
gga gct aaa gaa gga acg agt cag gaa gac att att cgt gct tgt gaa Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu 625 630 635 640			1920
att gct gaa atc cgc tcg gac att gaa caa atg cct cag ggc tat cag Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln 645 650 655			1968
aca gag tta tca gat ggt gcc ggt att tct ggc ggt caa aaa cag cgg Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg 660 665 670			2016
att gct tta gct agg gcc tta tta aca cag gca ccg gtt ttg att ctg Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu 675 680 685			2064
gat gaa gcc acc agc agt ctt gat att ttg aca gaa aag aaa att atc Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile 690 695 700			2112
agc aat ctc tta cag atg acg gag aaa aca ata att ttt gtt gcc cac Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His 705 710 715 720			2160
cgc tta agc att tca cag cgt act gac gaa gtc att gtc atg gat cag Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln 725 730 735			2208
gga aaa att gtt gaa caa ggc act cat aag gaa ctt tta gct aag caa Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln 740 745 750			2256

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 Gly Phe Tyr Tyr Asn Leu Phe Asn
 755 760

2280

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<211> 760

<212> PRT

<213> Streptococcus mutans

<400> 26

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Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser
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Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg
 35 40 45

His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala
 50 55 60

Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala
 65 70 75 80

Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu
 85 90 95

Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile
 100 105 110

Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe
 115 120 125

Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val
 130 135 140

Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser
 145 150 155 160

Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr
165 170 175

Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys
180 185 190

Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln
195 200 205

Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu
210 215 220

Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr
225 230 235 240

Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu
245 250 255

Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr
260 265 270

Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser
275 280 285

Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg
290 295 300

Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile
305 310 315 320

Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met
325 330 335

Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe
340 345 350

Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala
355 360 365

Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn
370 375 380

Ala Val Val Ser Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr
385 390 395 400

Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser
405 410 415

Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser
420 425 430

Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val
435 440 445

Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser
450 455 460

Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn
465 470 475 480

Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg
485 490 495

Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe
500 505 510

Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile
515 520 525

Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu
530 535 540

Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val
545 550 555 560

Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn
565 570 575

Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu
580 585 590

Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro
595 600 605

Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu

610	615	620
Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu		
625	630	635 640
Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln		
	645	650 655
Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg		
	660	665 670
Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu		
	675	680 685
Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile		
	690	695 700
Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His		
705	710	715 720
Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln		
	725	730 735
Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln		
	740	745 750
Gly Phe Tyr Tyr Asn Leu Phe Asn		
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<211> 900

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(900)

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cat aat ttt gcg aca cta tta att gtt cct ttg gtc tgc ttg att atc      96
His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile
          20          25          30

ttc ttg gtc ata ttc ctt tgt ttt gct aaa aaa gaa att aca gtg att      144
Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile
          35          40          45

tct act ggt gaa gtt gca cca aca aag gtt gta gat gtt atc caa tct      192
Ser Thr Gly Glu Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser
          50          55          60

tac agt gac agt tca atc att aaa aat aat tta gat aat aat gca gct      240
Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala
65          70          75          80

gtt gag aag gga gac gtt tta att gaa tat tca gaa aat gcc agt cca      288
Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro
          85          90          95

aac cgt cag act gaa caa aag aat att ata aaa gaa aga caa aaa cga      336
Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg
          100          105          110

gaa gag aag gaa aag aaa aaa cac caa aag agc aag aaa aag aag aag      384
Glu Glu Lys Glu Lys Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys
          115          120          125

tct aag agc aag aaa gct tcc aaa gat aag aaa aag aaa tcg aaa gac      432
Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Lys Ser Lys Asp
          130          135          140

aag gaa agc agc tct gac gat gaa aat gag aca aaa aag gtt tcg att      480
Lys Glu Ser Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile
145          150          155          160

ttt gct tca gaa gat ggt att att cat acc aat ccc aaa tat gat ggt      528
Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly
          165          170          175

gcc aat att att ccg aag caa acc gag att gct caa atc tat cct gat      576
Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp
          180          185          190

att caa aaa aca aga aaa gtg tta atc acc tat tat gct tct tct gat      624
Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp
          195          200          205

gat gtt gtt tct atg aaa aag ggg caa acc gct cgt ctt tcc ttg gaa      672
Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu
          210          215          220

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Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg
 100 105 110

Glu Glu Lys Glu Lys Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys
 115 120 125

Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Lys Ser Lys Asp
 130 135 140

Lys Glu Ser Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile
 145 150 155 160

Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly
 165 170 175

Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp
 180 185 190

Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp
 195 200 205

Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu
 210 215 220

Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val
 225 230 235 240

Ala Ser Ser Ala Thr Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr
 245 250 255

Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly
 260 265 270

Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp
 275 280 285

Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn
 290 295 300